

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF THE CLAIMS

1. (Currently Amended) An allelic classification method for categorizing a dataset comprising a plurality of datapoints, each datapoint comprising at least two numerical values, said method comprising the steps of:
 - (a) producing a plurality of angular values by calculating an angular value for each datapoint based on said datapoint's numerical values;
 - (b) sorting said plurality of datapoints by said angular values;
 - (c) producing a plurality of difference values by calculating differences between adjacent angular values;
 - (d) determining at least one category-dividing value by identifying at least one difference value above a predetermined threshold gap value; and
 - (e) classifying at least one datapoint according to its angular value relative to at least one category-dividing value.
2. (Original) The method of claim 1 wherein each datapoint comprises two numerical values.
3. (Original) The method of claim 2 wherein said angular value is an arctangent of said two numerical values.
4. (Original) The method of claim 1 wherein said numerical values represent fluorometric data.
5. (Original) The method of claim 1 wherein said determining step (d) identifies two category-dividing values.
6. (Original) The method of claim 1 further comprising the step of normalizing said numerical values to a scale.

7. (Original) The method of claim 6 wherein said scale ranges from 0.0 to 1.0.
8. (Original) The method of claim 1 further comprising the step of removing non-amplification datapoints from said dataset, said step comprising the steps of:
 - (i) calculating a Euclidean distance for each datapoint;
 - (ii) removing at least one datapoint from said dataset, wherein the Euclidean distance of said datapoint falls below a predetermined distance threshold.
9. (Original) The method of claim 1 wherein said determining step (d) identifies two category-dividing values comprising a first and a second category-dividing value, and said classifying step (e) comprises the steps of:
 - (i) classifying at least one datapoint in a first category, wherein all datapoints of said first category have an angular value lower than said first and second category-dividing values;
 - (ii) classifying at least one datapoint in a second category, wherein all datapoints of said second category have an angular value between said first and second category-dividing values; and
 - (iii) classifying at least one datapoint in a third category, wherein all datapoints of said third category have an angular value greater than said first and second category-dividing values.
10. (Original) The method of claim 9 wherein classification in said first category corresponds to homozygosity for a first allele, classification in said third category corresponds to homozygosity for a second allele, and classification in said second category corresponds to heterozygosity for said first and second alleles.
11. (Original) The method of claim 10 further comprising the step of determining the presence of a condition to bring to the attention of a human user, wherein said condition comprises the proportion of datapoints classified as heterozygous exceeding a predetermined threshold.

12. (Original) The method of claim 11 further comprising the step of determining the presence of a condition to bring to the attention of a human user.
13. (Original) The method of claim 12 wherein said condition comprises a substantial majority of datapoints being classified in one category.
14. (Original) The method of claim 13 wherein said category corresponds to heterozygosity for a first and second allele.
15. (Original) The method of claim 13 wherein said category corresponds to homozygosity for either a first or second allele.
16. (Original) The method of claim 13 wherein said category cannot be determined to correspond to either heterozygosity or homozygosity.
17. (Original) The method of claim 12 wherein said condition comprises said datapoints being classified into more than three categories.
18. (Original) The method of claim 12 wherein said condition comprises at least one of said datapoints remaining unclassified.
19. (Original) The method of claim 12 wherein said condition comprises the Euclidean distance between at least one of said classified datapoints and at least one non-amplification datapoint being below a predetermined threshold.
20. (Original) The method of claim 12 wherein said condition comprises a substantial majority of datapoints in said first category having an angular value higher than a predetermined threshold.
21. (Original) The method of claim 20 wherein said angular value is an arctangent and said predetermined threshold is 0.67.

22. (Original) The method of claim 12 wherein said condition comprises a substantial majority of datapoints in said third category having an angular value lower than a predetermined threshold.
23. (Original) The method of claim 22 wherein said angular value is an arctangent and said predetermined threshold is 1.0.
24. (Original) The method of claim 12 wherein said condition comprises a substantial majority of datapoints in said second category having an angular value lower than a first predetermined threshold or higher than a second predetermined threshold.
25. (Original) The method of claim 24 wherein said angular value is an arctangent, said first predetermined threshold is 0.18, and said second predetermined threshold is 1.35.
26. (Original) The method of claim 12 wherein said condition comprises the difference between the largest angular value of a datapoint in a category and the smallest angular value of a datapoint in the category exceeding a predetermined threshold.
27. (Original) The method of claim 26 wherein said angular value is an arctangent and said second predetermined threshold is 0.6.
28. (Original) The method of claim 12 wherein said first allele is a major allele and said second allele is a minor allele, and said major and minor alleles are in a Hardy-Weinberg equilibrium.
29. (Original) The method of claim 28 further comprising the step of determining the presence of a condition to bring to the attention of a human user, wherein said condition indicates an incompatibility with a Hardy-Weinberg equilibrium.

30. (Original) The method of claim 29 wherein said incompatibility comprises a greater number of datapoints classified as homozygous for said minor allele than classified as heterozygous.

31. (Original) The method of claim 12 further comprising the step of determining the presence of a condition to bring to the attention of a human user, said determining step comprising the steps of:

- (i) calculating the center of the set of removed datapoints, said center comprising an x and y coordinate; and
- (ii) determining if either said x or y coordinate exceeds a predetermined threshold.

32. (Original) The method of claim 31 wherein said predetermined threshold is 0.3 on a normalized scale of 0.0 to 1.0.

33. (Original) A method for performing allelic differentiation comprising:

acquiring fluorescence intensity data for a plurality of samples wherein the fluorescence intensity data is obtained by amplification of each sample in the presence of at least two fluorophore labels;

generating an angular value for each sample by comparing the fluorescence intensity obtained for the at least two fluorophore labels;

arranging the samples according to their angular value to form an angular-valued based distribution of the samples;

determining a difference value for each sample by taking the difference between the angular value for a selected sample and the angular value for an adjacent sample;

associating at least one difference value range with a selected allelic composition;

evaluating each sample's difference value with respect to the at least one difference value range to determine if the sample resides within the range; and

identifying the allelic composition of each sample on the basis of the difference value range which the sample resides within.

34. (Original) The method of Claim 33, wherein the allelic compositions comprises a homozygous allele.

35. (Original) The method of Claim 33, wherein the allelic compositions comprises a heterozygous allele.

36. (Original) The method of Claim 33, wherein the angular values for each sample are normalized.

37. (Original) The method of Claim 33, wherein the angular values are calculated as the arctangent between the at least two fluorophore labels.

38. (Original) The method of Claim 33, further comprising reducing the number of samples undergoing analysis by:

calculating a Euclidean distance for each sample; and

identifying a Euclidean distance threshold for which samples having a Euclidean distance below the threshold are removed from further analysis.

39. (Original) A method for genotypic analysis comprising:

amplifying a plurality of a genetic samples in the presence of at least two discriminable labels to thereby obtain intensity information indicative of the signals generated by the at least two discriminable labels during amplification;

calculating an angular value for each sample by comparing the intensity information for the at least two discriminable labels used during amplification;

ordering the samples on the basis of their angular value;

calculating a difference value for each sample by taking the difference between the angular value for a selected sample and the angular value for an adjacent sample;

identifying difference value ranges corresponding to homozygous and heterozygous allelic variations; and

determining whether a sample corresponds to a homozygous or heterozygous allelic variant by determining if the sample's difference value resides within the difference value ranges corresponding to homozygous or heterozygous allelic variation.

40. (Original) The method of Claim 39, wherein the angular values for each sample normalized prior to difference value determination.

41. (Original) The method of Claim 39, wherein the angular values are calculated as the arctangent between the at least two discriminable labels.